

Clone name	SEQ ID NO	Enantioselectivity for Neryl Butyrate (N) or Geranyl Butyrate (G)
1f15 (G2)	21	G
3C12	22	G
3N19 (G2)	23	G
G2.2	24	G
2C3	25	G
2F11	26	G
KV11 (6C7)	27	N
KV6 (3A1)	28	N
KV2 (2D1)	29	N
N2.5	30	N
KV5 (2H6)	31	N
3E5	32	G
G2.1	33	G
3H24 (G2)	34	G
KV10 (4G6)	35	N
KV12 (6D4)	36	N
N2.2	37	N
N2.3	38	N
N2.1	39	N
KV4 (2E12)	40	N
KV9 (4C6)	41	N
7D6	42	G
3F3	43	G
2D11 (G2)	44	G
3C23 (G2)	45	G
G2.3	46	G
2A3	47	G
2F4	48	G
2B9 (G2)	49	G
2C5	50	G
KV1 (2A6)	51	N
2D13 (G2)	52	G
3C8	53	G
2D5	54	G

FIGURE 1

Clone Name	E value for Neryl Butyrate	E value for Geranyl Butyrate
Exemplar (sgc2 and sgd2)	---	2.1
Exemplar (2h6)	1.4	---
Exemplar (14g14)	1.8	---
Exemplar (3f19a11)	2.2	(not tested)
Exemplar (3e5)	---	3.0
Exemplar (3n19)	---	3.8

FIGURE 2

SEQ: 001-405 (pumilus)	(1)	1	-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	75
SEQ: 002-406 (subtilis)	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCTGTTACATCGC	
SEQ: 003-402 (megat.)	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 004-400 (lentus)	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 005-396 (circul.)	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 006-392 (azotof.)	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 007-398 (firmus)	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 008-393 (badius)	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 009-Dc5h	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 010-Dc5f	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 011-Dc5c1	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 012-Dc5a2	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 013-Dc512	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCAGTCACATCGC	
SEQ: 014-Sga	(1)		ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATCTTGTGGCTTGCCTTAGTGTAGGTTCAAATAGC	
SEQ: 015-Sgc	(1)		ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATCTTGTGGCTTGCCTTAGTGTAGGTTCAAATAGC	
SEQ: 016-Sgd	(1)		ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATCTTGTGGCTTGCCTTAGTGTAGGTTCAAATAGC	
SEQ: 017-Sgf	(1)		ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATCTTGTGGCTTGCCTTAGTGTAGGTTCAAATAGC	
SEQ: 018-Sgh	(1)		ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATCTTGTGGCTTGCCTTAGTGTAGGTTCAAATAGC	
SEQ: 019-Mt2b1	(1)		ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATCTTGTGGCTTGCCTTAGTGTAGGTTCAAATAGC	
SEQ: 020-H2a	(1)		-----ATGAAATTTGTAAAAAGGAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG-TCTGTTACATCGC	

Figure 3a

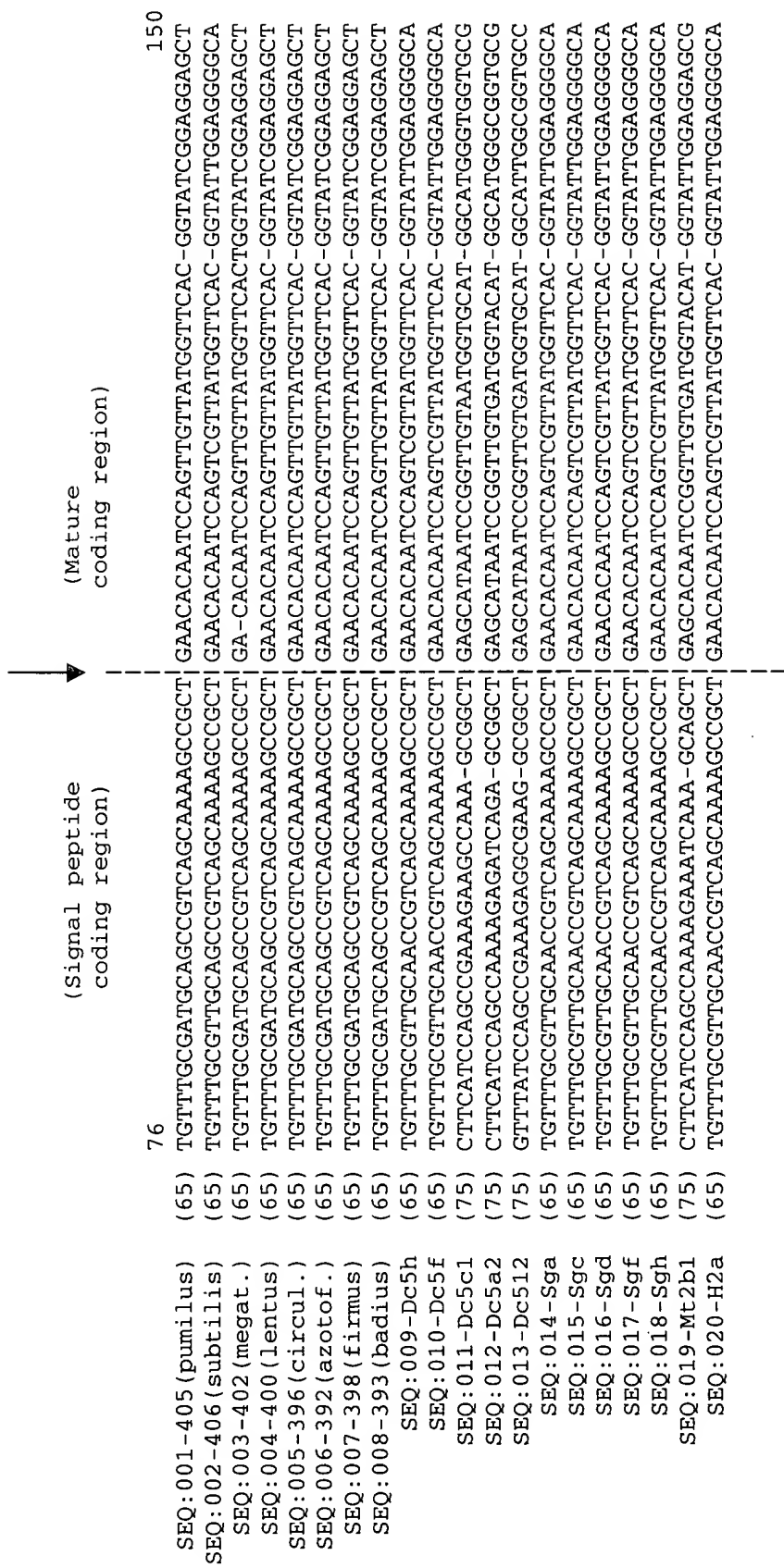


Figure 3b

SEQ: 001-405 (pumilus)	(139)	151	TCATACAAATTTTGC	225	TCATACAAATTTTGC
SEQ: 002-406 (subtilis)	(139)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 003-402 (megat.)	(139)		TCATACAAATTTTGC		TCATACAAATTTTGC
SEQ: 004-400 (lentus)	(139)		TCATACAAATTTTGC		TCATACAAATTTTGC
SEQ: 005-396 (circul.)	(139)		TCATACAAATTTTGC		TCATACAAATTTTGC
SEQ: 006-392 (azotof.)	(139)		TCATACAAATTTTGC		TCATACAAATTTTGC
SEQ: 007-398 (firmus)	(139)		TCATACAAATTTTGC		TCATACAAATTTTGC
SEQ: 008-393 (badius)	(139)		TCATACAAATTTTGC		TCATACAAATTTTGC
SEQ: 009-Dc5h	(139)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 010-Dc5f	(139)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 011-Dc5c1	(148)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 012-Dc5a2	(148)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 013-Dc512	(148)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 014-Sga	(139)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 015-Sgc	(139)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 016-Sgd	(139)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 017-Sgf	(139)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 018-Sgh	(139)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 019-Mt2b1	(148)		TCATTCAATTTTGC		TCATTCAATTTTGC
SEQ: 020-H2a	(139)		TCATTCAATTTTGC		TCATTCAATTTTGC

Figure 3c

SEQ: 001-405 (pumilus)	(214)	226	300
SEQ: 002-406 (subtilis)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAATGGCCCGGTATTATCACGATTTGTGTGCAAAAAGGTTTTAGACGAA	
SEQ: 003-402 (megat.)	(214)	TTTTGGGACAAAGACAGGACGACAAAATTATAACAATGGACCGGTATTACCACGATTTGTGCAAAAAGGTTTTAGATGAA	
SEQ: 004-400 (lentus)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAAGGTTTTAGACGAA	
SEQ: 005-396 (circul.)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAAGGTTTTAGACGAA	
SEQ: 006-392 (azotof.)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAAGGTTTTAGACGAA	
SEQ: 007-398 (firmus)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAAGGTTTTAGACGAA	
SEQ: 008-393 (badius)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAAGGTTTTAGACGAA	
SEQ: 009-Dc5h	(214)	TTCAAGGACAAAGACAGGACGACAAAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAAGGTTTTAGATGAA	
SEQ: 010-Dc5f	(214)	TTCTAAGACAAAAACAGGGAATAAACCGCAACAATGGTCCGCTCTATCAGATTCGTCAAAGATGTGTAGACAAA	
SEQ: 011-Dc5c1	(223)	TTCTATAGACAAAAACAGGCAATAAACCTAAACAATGGCCCGAGGCTCTCAGATTCGTGAAAGACGTACTAGCCAAA	
SEQ: 012-Dc5a2	(223)	TTCTATAGACAAAAACAGGTAATAAACCGCAACAATGGTCCGCTCTATCCAGATTCGTCAAAGATGTGTAGACAAA	
SEQ: 013-Dc512	(223)	TTCTATAGACAAAAACAGGAAATAAACCGCAACAATGGTCCGCTCTATCCAGATTCGTCAAAGATTCGTGTAGACAAA	
SEQ: 014-Sga	(214)	TTTCAGGACAAAGACAGGCAATAAATTAACAACGGTCCAGTATTATCGCGTTTCGTGAAAAAGGTTATAGATGAA	
SEQ: 015-Sgc	(214)	TTCTTGGGATAAGACAGGCAATAAATTAACAACGGTCCAGTATTATCGCGTTTCGTGAAAAAGGTTATAGATGAA	
SEQ: 016-Sgd	(214)	TTTAGTGTACAAAAACAGGCAATAAATTAACAACGGTCCAGTATTATCGCGTTTCGTGAAAAAGGTTATAGATGAA	
SEQ: 017-Sgf	(214)	TTCAAAAGACAAAGACAGGGAATAAACCGCAACAATGGTCCGCTCTATCCAGATTCGTCAAAGATGTGTAGACAAA	
SEQ: 018-Sgh	(214)	TTCTATTGACAAAGACAGGAAATAAACCGCAACAATGGTCCGCTCTATCCAGATTCGTCAAAGATGTGTAGACAAA	
SEQ: 019-Mt2b1	(223)	TTCTATAGACAAAAACAGGGAATAAACCGCAACAATGGTCCGCTCTGTTTATCTAGATTCGTCAAAGATGTGTAGACAAA	
SEQ: 020-H2a	(214)	TTTCAGGACAAAGACAGGAAATAAACCGCAACAATGGTCCGCTCTATCTAAATTCGTCAAAGATGTGTAGACAAA	

Figure 3d

SEQ: 001-405 (pumilus)	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGTATGGGTGGCGGAACACACACTTACTACATAAAAAATCTG	301
SEQ: 002-406 (subtilis)	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGGGCGGGAACACACTTTACTACATAAAAAATCTG	375
SEQ: 003-402 (megat.)	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTG	
SEQ: 004-400 (lentus)	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTG	
SEQ: 005-396 (circul.)	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTG	
SEQ: 006-392 (azotof.)	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTG	
SEQ: 007-398 (firmus)	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTG	
SEQ: 008-393 (badius)	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTG	
SEQ: 009-Dc5h	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGGGCGCGGAACACACTTTACTACATAAAAAATCTG	
SEQ: 010-Dc5f	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGTGGAGCGGAACACCGCTATATATCAAGAAATCTA	
SEQ: 011-Dc5c1	(298)	ACGGGCGCCAAAAAAGTGGATATTGTGCTCATAGTATGGGTGGAGCGGAACACCGCTATATATTAAGAAATCTA	
SEQ: 012-Dc5a2	(298)	ACAGGTGCCAAAAAAGTGGATATTGTGCTCATAGTATGGGTGGAGCGGAACACCGCTATATATTAAGAAATCTA	
SEQ: 013-Dc512	(298)	ACGGGTGCCAAAAAAGTGGATATTGTGCTCATAGTATGGGTGGAGCGGAACACCGCTATATATCAAGAAATCTA	
SEQ: 014-Sga	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGGGCGCTAACACGCTTTACTACATAAAAAATTTG	
SEQ: 015-Sgc	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGGGCGCTAACACGCTTTACTACATAAAAAATTTG	
SEQ: 016-Sgd	(289)	ACGGGTGCGAAAAAAGTGGATATTGTGCTCACAGCATGGGGGCGCTAACACGCTTTACTACATAAAAAATTTG	
SEQ: 017-Sgf	(289)	ACAGGAGCCAAAAAAGTGGATATTGTGCTCATAGTATGGGTGGAGCGGAACACATATATATTAAGAAATCTA	
SEQ: 018-Sgh	(289)	ACAGGAGCCAAAAAAGTGGATATTGTGCTCATAGTATGGGTGGAGCGGAACACATATATATTAAGAAATCTA	
SEQ: 019-Mt2b1	(298)	ACGGGTGCCAAAAAAGTGGATATTGTGCTCATAGTATGGGTGGAGCGGAACACCGCTATATATTAAGAAATCTA	
SEQ: 020-H2a	(289)	ACGGGTGCCAAAAAAGTGGATATTGTGCTCATAGTATGGGTGGAGCGGAACACCGCTATATATTAAGAAATCTA	

Figure 3e

376
SEQ:001-405 (pumilus) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGGCGCTTCCG
SEQ:002-406 (subtilis) (364) GACGGCGGAAATAAAAGTTGCAAAACGTCGTGACGCTTGGCGGCGGAAACCGTTTTCGACGACAGCAAGGCGCTTCCG
SEQ:003-402 (megat.) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGGAAACCGTTTTCGACGACAAAGCAAGGCGCTTCCG
SEQ:004-400 (lentus) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGGAAACCGTTTTCGACGACAAAGCAAGGCGCTTCCG
SEQ:005-396 (circul.) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGGAAACCGTTTTCGACGACAAAGCAAGGCGCTTCCG
SEQ:006-392 (azotof.) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGGAAACCGTTTTCGACGACAAAGCAAGGCGCTTCCG
SEQ:007-398 (firmus) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGGAAACCGTTTTCGACGACAAAGCAAGGCGCTTCCG
SEQ:008-393 (badius) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGGAAACCGTTTTCGACGACAAAGCAAGGCGCTTCCG
SEQ:009-Dc5h (364) GACGGCGGAAATAAAAGTTGAAAACGTCGTGACGCTTGGCGGCGGAAACCGTTTTCGACGACAGGCAAGGCGCTTCCG
SEQ:010-Dc5f (364) GATGGCGGCGATATAAAATTGAGAAACGTTGTACAAATTGGTGGAGCAAAACGGACTCGTTTTCAGCAGAGCATTTACCA
SEQ:011-Dc5c1 (373) GACGGTGGAGATATAAAATTGAAAACGTCGTACACATTTAGTGGAGCAAAACGGACTCGTATCAC'TCAGAGCATTTACCA
SEQ:012-Dc5a2 (373) GACGGCGGCGATATAAAATTGAAAACGTTGTACAAATTGGTGGAGCAAAACGGACTCGTTTTCAGCAGAGCATTTACCA
SEQ:013-Dc512 (373) GATGGCGGCGATATAAAATTGAGAAACGTTGTACAAATTGGTGGAGCAAAACGGACTCGTTTTCAGCAGAGCATTTACCA
SEQ:014-Sga (364) GATGGCGGTAATAAAATTGAAAACGTCGTAACACATTTGGCGGCGGAAATCGTCTTGTGACAGGCAAGGCGCTTCCG
SEQ:015-Sgc (364) GATGGCGGTAATAAAATTGAAAACGTCGTAACACATTTGGCGGCGGAAATCGTCTTGTGACAGGCAAGGCGCTTCCG
SEQ:016-Sgd (364) GATGGCGGTAATAAAATTGAAAACGTCGTAACACATTTGGCGGCGGAAATCGTCTTGTGACAGGCAAGGCGCTTCCG
SEQ:017-Sgf (364) GATGGTGGCGATATAAAATTGAGAAACGTTGTACAAATTGGTGGAGCAAAACGGACTCGTTTTCAGCAGAGCATTTACCA
SEQ:018-Sgh (364) GATGGTGGCGATATAAAATTGAGAAACGTTGTACAAATTGGTGGAGCAAAACGGACTCGTTTTCAGCAGAGCATTTACCA
SEQ:019-Mt2b1 (373) GATGGCGGCGATATAAAATTGAAAACGTCGTACCAATTTGGTGGAGCAAAACGGACTCGTTTTCAGCAGAGCATTTACCA
SEQ:020-H2a (364) GATGGCGGCGATATAAAATTGAGAAACGTTGTACAAATTGGCGGAGCAAAACGGACTCGTTTTCAGCAGAGCATTTACCA

Figure 3f

525

451

SEQ: 001-405 (pumilus) (439) GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 002-406 (subtilis) (439) GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 003-402 (megat.) (439) GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 004-400 (lentus) (439) GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 005-396 (circul.) (439) GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 006-392 (azotof.) (439) GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 007-398 (firmus) (439) GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 008-393 (badius) (439) GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 009-Dc5h (439) GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 010-Dc5f (439) GGCACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 011-Dc5c1 (448) GGCACCGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCTCAGCAGATCTTATTTGTCGTCACAGCCCT
 SEQ: 012-Dc5a2 (448) GGCACCGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCTCAGCAGATCTTATTTGTCGTCACAGCCCT
 SEQ: 013-Dc512 (448) GGCACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA - GCTCAGCAGATCTTATTTGTCGTCACAGCCCT
 SEQ: 014-Sga (439) GGTACTGATCCCAACCAAAAGATTTTGTACACATCCGTTTACA - GTAGTGCCTGATATGATGTGTATGAATTACTTT
 SEQ: 015-Sgc (439) GGTACTGATCCCAACCAAAAGATTTTGTACACATCCGTTTACA - GTAGTGCCTGATATGATGTGTATGAATTACTTT
 SEQ: 016-Sgd (439) GGTACTGATCCCAACCAAAAGATTTTGTACACATCCGTTTACA - GTAGTGCCTGATATGATGTGTATGAATTACTTT
 SEQ: 017-Sgf (439) GGCACAGATCCAAATCAAAAGATTTTATACACATCCGTTTACA - GCTCAGCAGATCTTATTTGTCGTCACAGTCTT
 SEQ: 018-Sgh (439) GGCACAGATCCAAATCAAAAGATTTTATACACATCCGTTTACA - GCTCAGCAGATCTTATTTGTCGTCACAGTCTT
 SEQ: 019-Mt2b1 (448) GGAACAGATCCAAATCAAAAGATTTCTATACATCTGTCTATA - GCTCAGCCGATTTGATTTGTCGTCACAGCCCT
 SEQ: 020-H2a (439) GGCACAGATCCAAATCAAAAGATTTCTTATACACATCCGTTTACAAGCTCAGCCGATCTCATTTGTCGTCACAGTCTT

Figure 39

526 600

SEQ: 001-405 (pumilus) (513) ATCAAAATTAGACGGT-GCTAAAAAC-GCTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA

SEQ: 002-406 (subtilis) (513) ATCAAGATTAGATGGT-GCTAGAAAC-GTTCAAAATCCATGGCGTTGGACACATCGGCCTTCTGTACAGCAGCCAA

SEQ: 003-402 (megat.) (513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA

SEQ: 004-400 (lentus) (513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA

SEQ: 005-396 (circul.) (513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA

SEQ: 006-392 (azotof.) (513) ATCAAAATTAGACGGT-GCTAAAAAC-GTACAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA

SEQ: 007-398 (firmus) (513) ATCAAAATTAGACGGT-GCTAAAAAC-GCTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA

SEQ: 008-393 (badius) (513) ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA

SEQ: 009-Dc5h (513) ATCAAGATTAGATGGT-GCGAGAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAA

SEQ: 010-Dc5f (513) CTCCTCGTTTAAATTGGC-GCAAGAAAC-ATCCTGATCCATGGCGTTGGTCATATCGGCTTATTAACCTCAAGCCAA

SEQ: 011-Dc5c1 (522) TTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTGTATCCACGGCGTTGGACATATCGGTCATTAACCTCAAGCCAA

SEQ: 012-Dc5a2 (522) CTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTGTATCCACGGCGTTGGTCATATCGGTCATTAACCTCAAGCCAA

SEQ: 013-Dc512 (522) CTCCTCAGTTTAAATTGGCGCAAGAAAC-ATCCTGATCCA-GGCGTTGGTCATATCGGTCATTAACCTCAAGCCAA

SEQ: 014-Sga (513) AACAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCTTCTGTACAGCAGCCAA

SEQ: 015-Sgc (513) ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCTTCTGTACAGCAGCCAA

SEQ: 016-Sgd (513) ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCTTCTGTACAGCAGCCAA

SEQ: 017-Sgf (513) CTCCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAATTCATGGCGTTGGACATATCGGTCATTAACCTCAAGCCAA

SEQ: 018-Sgh (513) CTCCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAATTCATGGCGTTGGACATATCGGTCATTAACCTCAAGCCTA

SEQ: 019-Mt2b1 (522) TTCGC-GTTTAACTGGCGCAAGAAAT-GTCTGTATCCACGGCGTTGGCCATATCGGTCATTAACCTCAAGCCAA

SEQ: 020-H2a (514) CTCCTCGTTTAAATTGGCTGCAAGAAACAGTCCAAATCCATGGCGTTGGACATATCGGTCATTAACCTCAAGCCAA

Figure 3h

SEQ: 021-1f15 (G2)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 022-3C12	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 023-3N19 (G2)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 024-G2.2	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 025-2C3	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 026-2F11	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 027-KV1.1 (6C7)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 028-KV6 (3A1)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 029-KV2 (2D1)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGAGCTTCAATACAGTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 030-N2.5	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGAGCTTCAATACAGTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 031-KV5 (2H6)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 032-3E5	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 033-G2.1	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 034-3H24 (G2)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 035-KV10 (4G6)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 036-KV12 (6D4)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 037-N2.2	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 038-N2.3	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 039-N2.1	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 040-KV4 (2E12)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 041-KV9 (4C6)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 042-7D6	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 043-3F3	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 044-2D1.1 (G2)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 045-3C23 (G2)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 046-G2.3	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 047-2A3	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 048-2F4	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 049-2B9 (G2)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 050-2C5	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 051-KV1 (2A6)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 052-2D1.3 (G2)	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 053-3C8	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT
SEQ: 054-2D5	(1) TGAACACAAATCCAGTTGTTATGGTTTCACGGTATTCGGAGGGGCATCATCTCAATTTTTCGGGGAAATTTAAGAGCATTATCT

Figure 4a

151 (151) SEQ: 021-1f15 (G2) TGGCCCGGTATTATCGCGTTTGTGAAAAAGGTATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 022-3C12 (151) TGGCCCGGTATTATCTAGATTCTGTCAAAGATGTGCTAGACAAAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 023-3N19 (G2) (151) TGGCCCGGTATTATCACGATTTGTGAAAAAGGTATTAGATGAAACCGGTGCGAAAAAAGTGGACATTGTGCGCTCA

SEQ: 024-G2.2 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 025-2C3 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 026-2F11 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 027-KV11 (6C7) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 028-KV6 (3A1) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 029-KV2 (2D1) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 030-N2.5 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 031-KV5 (2H6) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 032-3E5 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGACATTGTGCGCTCA

SEQ: 033-G2.1 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGACATTGTGCGCTCA

SEQ: 034-3H24 (G2) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 035-KV10 (4G6) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 036-KV12 (6D4) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 037-N2.2 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 038-N2.3 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 039-N2.1 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 040-KV4 (2E12) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 041-KV9 (4C6) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 042-7D6 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 043-3F3 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 044-2D11 (G2) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 045-3C23 (G2) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 046-G2.3 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 047-2A3 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 048-2F4 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 049-2B9 (G2) (151) TGGCCCGGTATTATCGCGTTTGTGAAAAAGGTATTAGATGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 050-2C5 (151) TGGCCCGGTATTATCGCGTTTGTGAAAAAGGTATTAGATGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 051-KV1 (2A6) (151) TGGCCCGGTATTATCACGATTTGTGAAAAAGGTATTAGATGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 052-2D13 (G2) (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 053-3C8 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 054-2D5 (151) TGGCCCGGTATTATCACGATTTGTGCAAAAAGTTTGTAGACGAAACCGGTGCGAAAAAAGTGGATATTGTGCGCTCA

Figure 4 c

226 226 CAGCATGGGCGGCGCTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 021-1f15 (G2) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 022-3C12 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 023-3N19 (G2) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 024-G2.2 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 025-2C3 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 026-2F11 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 027-KV11 (6C7) (226) CAGTATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 028-KV6 (3A1) (226) CAGTATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 029-KV2 (2D1) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 030-N2.5 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 031-KV5 (2H6) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 032-3E5 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 033-G2.1 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 034-3H24 (G2) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 035-KV10 (4G6) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 036-KV12 (6D4) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 037-N2.2 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 038-N2.3 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 039-N2.1 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 040-KV4 (2E12) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGAAATATAAGTTGAAAAACGTCGTAAC
 SEQ: 041-KV9 (4C6) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGATGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 042-7D6 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 043-3F3 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 044-2D11 (G2) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 045-3C23 (G2) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 046-G2.3 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 047-2A3 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 048-2F4 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 049-2B9 (G2) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 050-2C5 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 051-KV1 (2A6) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 052-2D13 (G2) (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 053-3C8 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC
 SEQ: 054-2D5 (226) CAGCATGGGCGGCGGAAACACACTTTTACTACATAAAAAATCTGGACGGCGGTAATAAGTTGAAAAACGTCGTAAC

Figure 4 d

301 375

SEQ: 021-1f15 (G2) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 022-3C12 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 023-3N19 (G2) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 024-G2.2 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 025-2C3 (301) CATTTGGTGAGCAAAACGGACTCGTTTCAAGCAGAGCATTACAGGCACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 026-2F11 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 027-KV11 (6C7) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAAGATTTGTACAC
 SEQ: 028-KV6 (3A1) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAAGATTTGTACAC
 SEQ: 029-KV2 (2D1) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAACCAAAAAGATTTGTACAC
 SEQ: 030-N2.5 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAACCAAAAAGATTTGTACAC
 SEQ: 031-KV5 (2H6) (301) GCTTGGCGGCACGAATCGTCTTGTAAACAGGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTGTACGC
 SEQ: 032-3E5 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 033-G2.1 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 034-3H24 (G2) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 035-KV10 (4G6) (301) ACTTGGCGGCACGAATCGTCTTGTAAACAGGCAAGGCGCTTCCGGGAACAGATCCCAACCAAAAAGATTTTATACAC
 SEQ: 036-KV12 (6D4) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 037-N2.2 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 038-N2.3 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 039-N2.1 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 040-KV4 (2E12) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 041-KV9 (4C6) (301) ACTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAAGATTTGTACAC
 SEQ: 042-7D6 (301) ACTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 043-3F3 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 044-2D11 (G2) (301) ACTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 045-3C23 (G2) (301) ACTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 046-G2.3 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 047-2A3 (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAAGATTTGTACAC
 SEQ: 048-2F4 (301) ACTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 049-2B9 (G2) (301) ACTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 050-2C5 (301) ACTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAACCAAAAAGATTTTATACAC
 SEQ: 051-KV1 (2A6) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAAGATTTTATACAC
 SEQ: 052-2D13 (G2) (301) GCTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGTACTGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 053-3C8 (301) ACTTGGCGGCACGAATCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC
 SEQ: 054-2D5 (301) ACTTGGCGGCACGAACCGTTCGACGACAAAGCAAGGCGCTTCCGGGAACAGATCCCAATCAAAAAGATTTTATACAC

Figure 4e

376
 SEQ: 021-1f15 (G2) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAATGTTCAAAAT
 SEQ: 022-3C12 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGGGC'TAAAAATGTTCAAAAT
 SEQ: 023-3N19 (G2) (376) ATCCATTACGGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 024-G2.2 (376) ATCCATTACGGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 025-2C3 (376) ATCCGTCATAGTCTCAGCAGATCTTATTTGTCGTCACAGTCTCTCTCGTTTAAATTTGGCGCAAGAAACGTTCCAAAT
 SEQ: 026-2F11 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 027-KV11 (6C7) (376) ATCCGTTTACAGTAGTGTGATATGATGTGATGAATTAATTAATCAAAATTAGACGGGGC'TAAAAATGTTCAAAAT
 SEQ: 028-KV6 (3A1) (376) ATCCGTTTACAGTAGTGTGATATGATGTGATGAATTAATTAATCAAAATTAGACGGGGC'TAAAAATGTTCAAAAT
 SEQ: 029-KV2 (2D1) (376) ATCCGTTTACAGTAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGGGC'TAAAAATGTTCAAAAT
 SEQ: 030-N2.5 (376) ATCCGTTTACAGTAGTGTGATATGATGTGATGAATTAATTAATCAAAATTAGACGGGGC'TAAAAATGTTCAAAAT
 SEQ: 031-KV5 (2H6) (376) ATCCGTTTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 032-3E5 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGGGC'TAAAAATGTTCAAAAT
 SEQ: 033-G2.1 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 034-3H24 (G2) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 035-KV10 (4G6) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 036-KV12 (6D4) (376) ATCCGTTTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 037-N2.2 (376) ATCCGTTTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 038-N2.3 (376) ATCCGTTTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 039-N2.1 (376) ATCCGTTTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 040-KV4 (2E12) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 041-KV9 (4C6) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGGGC'TAAAAATGTTCAAAAT
 SEQ: 042-7D6 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 043-3F3 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 044-2D11 (G2) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 045-3C23 (G2) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 046-G2.3 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 047-2A3 (376) ATCCGTTTACAGTAGTGTGATATGATGTGATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 048-2F4 (376) ATCCGTTTACAGTAGTGTGATATGATGTGATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 049-2B9 (G2) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGGGC'TAAAAATGTTCAAAAT
 SEQ: 050-2C5 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 051-KV1 (2A6) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 052-2D13 (G2) (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAATGTTCAAAAT
 SEQ: 053-3C8 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAACGTTCAAAAT
 SEQ: 054-2D5 (376) ATCCATTACAGCAGTCCGATATGATGTCAATGAATTAATTAATCAAAATTAGACGGTGC'TAAAAATGTTCAAAAT

Figure 4f

451
 SEQ: 021-1f15 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 022-3C12 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 023-3N19 (G2) (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 024-G2.2 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 025-2C3 (451) CCATGGCGTTGGACATATCGGTCATTAAACCTCAAGCCAAAGTCAAGAGGATATATTAAAGAAAGGCTTTAACGGCGG
 SEQ: 026-2F11 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAAGAGGATATATTAAAGAAAGGACTGAACGGCGG
 SEQ: 027-KV11 (6C7) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 028-KV6 (3A1) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 029-KV2 (2D1) (451) TCATGGTGTGCGACATATCGGCCCTTCTGTACAGCAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 030-N2.5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 031-KV5 (2H6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 032-3E5 (451) CCATGGCGTTGGGCACATTTGGCCCTTCTGTACAGCAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 033-G2.1 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 034-3H24 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 035-KV10 (4G6) (451) TCATGGCGTTGGGCACATTTGGCCCTTCTGTATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 036-KV12 (6D4) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 037-N2.2 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 038-N2.3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 039-N2.1 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 040-KV4 (2E12) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 041-KV9 (4C6) (451) TCATGGTGTGCGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 042-7D6 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 043-3F3 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 044-2D11 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 045-3C23 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 046-G2.3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 047-2A3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 048-2F4 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 049-2B9 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 050-2C5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 051-KV1 (2A6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 052-2D13 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 053-3C8 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 054-2D5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG

Figure 4g

SEQ: 021-1f15 (G2)	(526)	GGGACTCAATACGAATTGA	526	544
SEQ: 022-3C12	(526)	GGGACTCAATACGAATTGA		
SEQ: 023-3N19 (G2)	(526)	GGGACTGAATACAAAATTGA		
SEQ: 024-G2.2	(526)	GGGACTCAATACGAATTGA		
SEQ: 025-2C3	(526)	GGCCACAAATACGAATTGA		
SEQ: 026-2F11	(526)	AGGCTAAATACGAATTGA		
SEQ: 027-KV11 (6C7)	(526)	GGGCTAAATACAAAATTGA		
SEQ: 028-KV6 (3A1)	(526)	GGGCTAAATACAAAATTGA		
SEQ: 029-KV2 (2D1)	(526)	GGGCCAAAAATACAAAATTGA		
SEQ: 030-N2.5	(526)	GGGCCACAAATACAAAATTGA		
SEQ: 031-KV5 (2H6)	(526)	GGGCTGAATACAAAATTGA		
SEQ: 032-3E5	(526)	GGGCTCAATACGAATTGA		
SEQ: 033-G2.1	(526)	GGGACTCAATACGAATTGA		
SEQ: 034-3H24 (G2)	(526)	GGGACTCAATACGAATTGA		
SEQ: 035-KV10 (4G6)	(526)	GGGCCACAAATACAAAATTGA		
SEQ: 036-KV12 (6D4)	(526)	AGGCCACAAATACAAAATTGA		
SEQ: 037-N2.2	(526)	AGGCCACAAATACAAAATTGA		
SEQ: 038-N2.3	(526)	AGGCCACAAATACAAAATTGA		
SEQ: 039-N2.1	(526)	AGGCCACAAATACAAAATTGA		
SEQ: 040-KV4 (2E12)	(526)	GGGCCACAAATACAAAATTGA		
SEQ: 041-KV9 (4C6)	(526)	GGGCCACAAATACGAATTGA		
SEQ: 042-7D6	(526)	GGGATTAATACGAATTGA		
SEQ: 043-3F3	(526)	GGCCAGAAATACGAATTGA		
SEQ: 044-2D11 (G2)	(526)	AGGCCAGAAATACGAATTGA		
SEQ: 045-3C23 (G2)	(526)	GGGCCACAAATACGAATTGA		
SEQ: 046-G2.3	(526)	GGGCCAGAAATACGAATTGA		
SEQ: 047-2A3	(526)	AGGCTAAATACAAAATTGA		
SEQ: 048-2F4	(526)	AGGCCAGAAATACGAATTGA		
SEQ: 049-2B9 (G2)	(526)	AGGCCAAAAATACGAATTGA		
SEQ: 050-2C5	(526)	AGGCCAAAAATACGAATTGA		
SEQ: 051-KV1 (2A6)	(526)	GGGCCAGAAATACGAATTGA		
SEQ: 052-2D13 (G2)	(526)	AGGCCAAAAATACGAATTGA		
SEQ: 053-3C8	(526)	GGGCCAAAAATACAAAATTGA		
SEQ: 054-2D5	(526)	AGGACAAAAATACAAAATTGA		

Figure 4 h

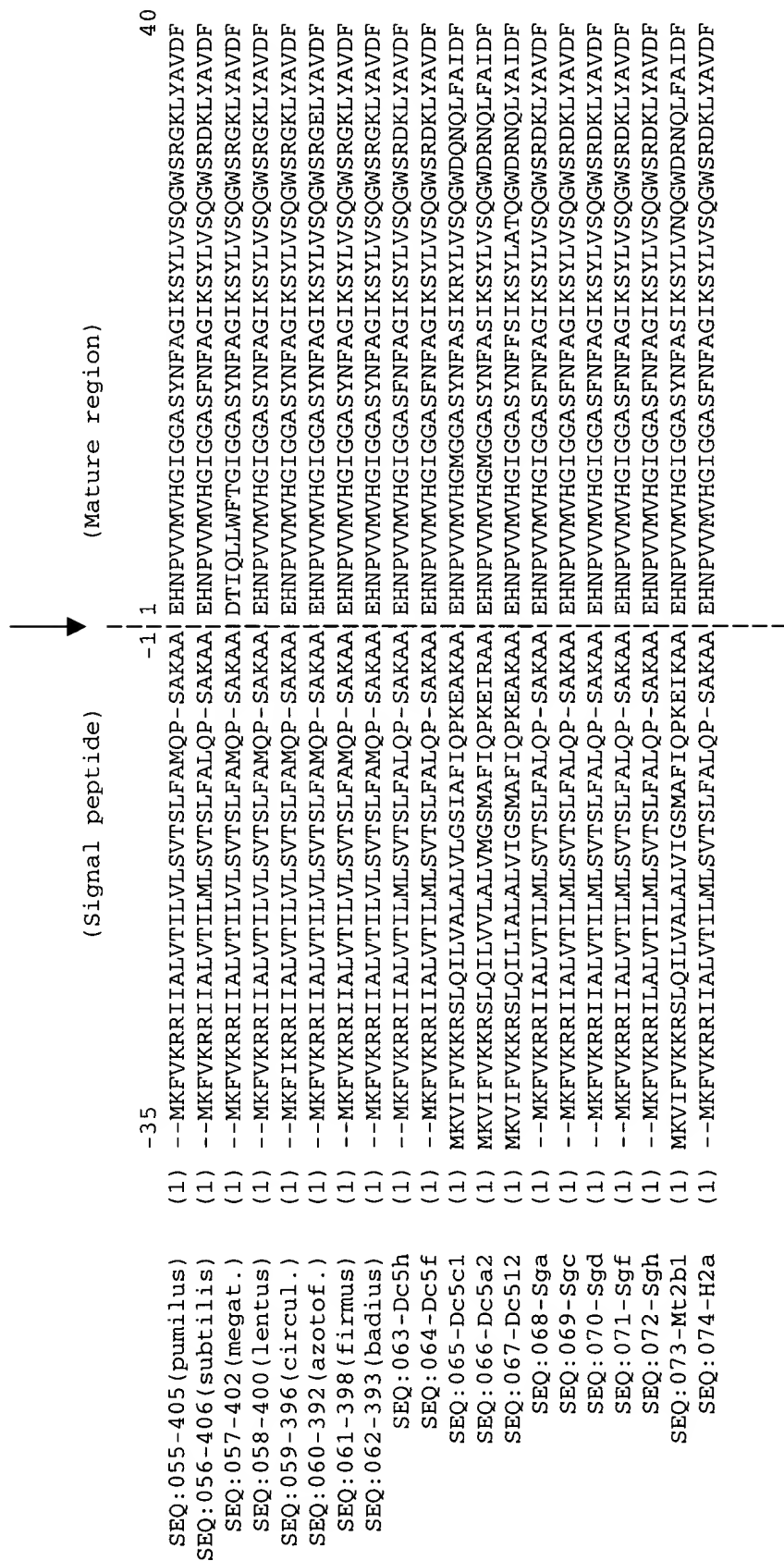


Figure 5a

SEQ: 055-405 (pumilus)	(73)	WDKTGTNNNGPVL	SRFVQKVL	DETGA	KKVD	IVAHSMGGANT	PYYIKNLDGGNKI	ENVVTLGGANRSTTSKALPG	41	115
SEQ: 056-406 (subtilis)	(73)	WDKTGTNNNGPVL	PRFVQKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKVANVVTLGGANRLTTGKALPG			
SEQ: 057-402 (megat.)	(73)	WDKTGTNNNGPVL	SRFVQKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLTTSKALPG		
SEQ: 058-400 (lentus)	(73)	WDKTGTNNNGPVL	SRFVQKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLTTSKALPG		
SEQ: 059-396 (circul.)	(73)	WDKTGTNNNGPVL	SRFVQKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLTTSKALPG		
SEQ: 060-392 (azotof.)	(73)	WDKTGTNNNGPVL	SRFVQKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLTTSKALPG		
SEQ: 061-398 (firmus)	(73)	WDKTGTNNNGPVL	SRFVQKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLTTSKALPG		
SEQ: 062-393 (badius)	(73)	WDKTGTNNNGPVL	SRFVQKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLTTSKALPG		
SEQ: 063-Dc5h	(73)	KDKTGTNNNGPVL	SRFVQKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLTTGKALPG		
SEQ: 064-Dc5f	(73)	XDKTGNNRNNGPRL	SRFVKDVL	DKTGA	KKVD	IVAHSMGGANT	LYYIKNLDGGDKI	ENVVTLGGANGLVSSRALPG		
SEQ: 065-Dc5c1	(76)	IDKTGNNLNNGPRL	SRFVKDVL	AKTGA	KKVD	IVAHSMGGANT	LYYIKNLDGGDKI	ENVVTLGGANGLVSLRALPG		
SEQ: 066-Dc5a2	(76)	IDKTGNNRNNGPRL	SRFVKDVL	AKTGA	KKVD	IVAHSMGGANT	LYYIKNLDGGDKI	ENVVTLGGANGLVSLRALPG		
SEQ: 067-Dc512	(76)	IDKTGNNRNNGPRL	SRFVKDVL	DKTGA	KKVD	IVAHSMGGANT	LYYIKNLDGGDKI	ENVVTLGGANGLVSSRALPG		
SEQ: 068-Sga	(73)	RDKTGNNLNNGPVL	SRFVKKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLVTGKALPG		
SEQ: 069-Sgc	(73)	WDKTGNNLNNGPVL	SRFVKKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLVTGKALPG		
SEQ: 070-Sgd	(73)	SDKTGNNLNNGPVL	SRFVKKVL	DETGA	KKVD	IVAHSMGGANT	LYYIKNLDGGNKI	ENVVTLGGANRLVTGKALPG		
SEQ: 071-Sgf	(73)	KDKTGNNRNNGPRL	SRFVKDVL	DKTGA	KKVD	IVAHSMGGANT	LYYIKNLDGGDKI	ENVVTLGGANGLVSSRALPG		
SEQ: 072-Sgh	(73)	IDKTGNNRNNGPRL	SRFVKDVL	DKTGA	KKVD	IVAHSMGGANT	LYYIKNLDGGDKI	ENVVTLGGANGLVSSRALPG		
SEQ: 073-Mt2b1	(76)	IDKTGNNRNNGPRL	SRFVKDVL	DKTGA	KKVD	IVAHSMGGANT	LYYIKNLDGGDKI	ENVVTLGGANGLVSLRALPG		
SEQ: 074-H2a	(73)	RDKTGNNRNNGPRL	SKFVKDVL	DKTGA	KKVD	IVAHSMGGANT	LYYIKNLDGGDKI	ENVVTLGGANGLVSSRALPG		

Figure 5b

SEQ: 055-405 (pumilus)	(148)	116	TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGQNTN	181
SEQ: 056-406 (subtilis)	(148)		TDPNQKILYTSIYSSADMIVN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN	
SEQ: 057-402 (megat.)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 058-400 (lentus)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 059-396 (circul.)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 060-392 (azotof.)	(148)		TDPNQKILYTSIYSSANMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGLDNTN	
SEQ: 061-398 (firmus)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 062-393 (badius)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 063-Dc5h	(148)		TDPNQKILYTSIYSSADMIVMN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN	
SEQ: 064-Dc5f	(148)		TDPNQKILYTSIYSSADLIIVN- SLRSLIGARNVLIHGVGHI GLLTSSQVKGVIKEGLNGGGLNTN	
SEQ: 065-Dc5c1	(151)		TDPNQKILYTSIYSSADLIIVN- SLRSLIGARNVLIHGVGHI GLLTSSQVKGVIKEGLNGGGQNTN	
SEQ: 066-Dc5a2	(151)		TDPNQKILYTSIYSSADLIIVN- SLRSLIGARNVLIHGVGHI GLLTSSQVKGVIKEGLNGGGQNTN	
SEQ: 067-Dc512	(151)		TDPNQKILYTSIYSSADLIIVN- SLRSLIGARNVLIHGVGHI GLLTSSQVKGVIKEGLNGGGGLNTN	
SEQ: 068-Sga	(148)		TDPNQKILYTSIYSSADMIVMN- YLTKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 069-Sgc	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 070-Sgd	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 071-Sgf	(148)		TDPNQKILYTSIYSSADLIIVN- SLRSLIGARNVQIHGVGHI GLLTSSQVKGVIKEGLNGGGLNTN	
SEQ: 072-Sgh	(148)		TDPNQKILYTSIYSSADLIIVN- SLRSLIGARNVQIHGVGHI GLLTSSQVKGVIKEGLNGGGQNTN	
SEQ: 073-Mt2b1	(151)		TDPNQKILYTSIYSSADLIIVN- SLRSLIGARNVLIHGVGHI GLLTSSQVKGVIKEGLNGGGLNTN	
SEQ: 074-H2a	(148)		TDPNQKILYTSIYKLSRSHCRQQLSFNWLQETVQIHGVGHI GLLTSSQVKGVIKEGLNGGGGLNTN	

Figure 5c

SEQ: 075 - 1f15 (G2)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGTNRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	150
SEQ: 076 - 3C12	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 077 - 3N19 (G2)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYGSADMIMVNYLSKLDGAKNVQI	
SEQ: 078 - G2. 2	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYGSADMIMVNYLSKLDGAKNVQI	
SEQ: 079 - 2C3	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANGLVSSRALPGTDPNQKILYTSIYSSADLIIVNLSRLIGARNVQI	
SEQ: 080 - 2F11	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSRALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 081 - KV11 (6C7)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 082 - KV6 (3A1)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 083 - KV2 (2D1)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 084 - N2. 5	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 085 - KV5 (2H6)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLVTGKALPGTDPNQKILYASVYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 086 - 3E5	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 087 - G2. 1	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGTNRLTTSRALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 088 - 3H24 (G2)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 089 - KV10 (4G6)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLVTGKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 090 - KV12 (6D4)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 091 - N2. 2	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 092 - N2. 3	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 093 - N2. 1	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 094 - KV4 (2E12)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 095 - KV9 (4C6)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 096 - 7D6	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 097 - 3F3	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 098 - 2D11 (G2)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 099 - 3C23 (G2)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 100 - G2. 3	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 101 - 2A3	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 102 - 2F4	(76)	SMGGANTLYYIKNLDGGDKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 103 - 2B9 (G2)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 104 - 2C5	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 105 - KV1 (2A6)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 106 - 2D13 (G2)	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 107 - 3C8	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	
SEQ: 108 - 2D5	(76)	SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIMVNYLSKLDGAKNVQI	

Figure 6b

	151		180
SEQ: 075-1f15 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 076-3C12	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 077-3N19 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 078-G2.2	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 079-2C3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 080-2F11	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 081-KV11 (6C7)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 082-KV6 (3A1)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 083-KV2 (2D1)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 084-N2.5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 085-KV5 (2H6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 086-3E5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 087-G2.1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 088-3H24 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 089-KV10 (4G6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 090-KV12 (6D4)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 091-N2.2	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 092-N2.3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 093-N2.1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 094-KV4 (2E12)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 095-KV9 (4C6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 096-7D6	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 097-3F3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 098-2D11 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 099-3C23 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 100-G2.3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 101-2A3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 102-2F4	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 103-2B9 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 104-2C5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 105-KV1 (2A6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 106-2D13 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 107-3C8	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	
SEQ: 108-2D5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	

Figure 6c